G A G AAG n n n n ↕ n (SEQ ID NO: 2)

where the recognition sequence is -C-T-C-T-T-C-, N and n represent complementary, ambiguous base pairs and the arrows indicate the cleavage sites in each strand. As the example illustrates, the recognition sequence is non-palindromic, and the cleavage occurs outside of that recognition site.

Please delete the paragraph beginning on page 25, line 3 and replace with the following:

Adaptor sequences containing PCR primer template sequences were then ligated to the purified fragments using 100U T4 ligase in 1x T4 DNA ligase buffer (New England Biolabs) at 16 °C overnight. The adaptor sequences were 5'-d(pAATTCGAACCCCTTCGGATC)-3' (SEQ ID NO: 3) and 5'-d(GATCCGAAGGGGTTCGAATT)-3' (SEQ ID NO: 4) (Figure 2, Step 4) The ligase was then heat inactivated at 65 °C for 15 minutes.

Please delete the paragraph beginning on page 25, line 8 and replace with the following:

The fragments were then subjected to PCR with one primer that corresponded to the PCR primer template sequence 5'-d(GATCCGAAGGGGTTCGAATT)-3' (SEQ ID NO: 5) (Figure 2, Step 5). The PCR mixture contained approx. 1 ng ligated DNA fragments, 5 units AmpliTaq Gold polymerase (Perkins Elmer), 5 uM pimer, 200uM dNTPs, 15 mM Tris-HCl (pH8.2), 50 mM KCl, 2.5 mM $MgCl_2$ in a final volume of 50 ul. PCR was performed in a Perkin-Elmer 9600 thermocycler using an initial 10 minute denaturation at 95 °C, 35 cycles of a 1 minute denaturation at 94 °C, annealing for 1 minute at 57 °C and extension at 72 °C for 2 minutes. This is followed by a final 5 minute extension cycle at 72 °C.

Please delete the paragraph beginning on page 26, line 22 and replace with the following:

Adaptors containing PCR primer template sequences were ligated in a 50 ul mixture of 400 ng digested genomic DNA, 10 pmol adaptor and 40 unit T4 ligase in a 1X T4 ligase buffer. (Figure 3, Step 2) The adaptor sequences were as follows: 5'-d(pATNNGATCCGAAGGGTTCGAATTC)-3' (SEQ ID NO: 6) and 5'(GAATTCGAACCCCTTCGGATC)-3' (SEQ ID NO: 7). The ligation was conducted at 16°C overnight. The ligase was inactivated by incubation at 65°C for 15 minutes.

Please delete the paragraph beginning on page 26, line 28 and replace with the following:

The fragments were then subjected to PCR with one primer that corresponded to the PCR primer template sequence: 5'-(GAATTCGAACCCCTTCGGATC)-3' (SEQ ID NO: 8) in a 50 ul reaction containing 20 ng ligated DNA, 1 unit AmpliTaq Gold polymerase (Perkins Elmer), 3 uM primer, 200uM dNTPs, 15 mM Tris-HCl (pH8.0), 50 mM KCl, 2.5 mM $MgCl_2$. PCR was performed in a Perkin-Elmer 9600 thermocycler using an initial 10 minute denaturation at 95°C, 35 cycles of a 0.5 minute denaturation at 94°C, annealing for 0.5 minute at 57°C and extension at 72°C for 2 minutes. This is followed by a final 5 minute extension cycle at 72°C.

Please delete the paragraph beginning on page 27, line 14 and replace with the following:

The restriction fragments were then ligated to adaptor sequences. The ligation mixture contained: 5 pmol Eco R I adaptor [5'-d(pAATTCGAACCCCTTCGGATC)-3' (SEQ ID NO: 9) and 5'-d(GATCCGAAGGGGTTCG)-3' (SEQ ID NO: 10)], 50 pmol Sau3A I adaptor [5'-d(pGATCGCCCTATAGTGAGTCGTATTACAGTGGACCATCGAGGGTCA)-3' (SEQ ID NO: 11)], 5 mM DTT, 0.5 ng/ul BSA, 100 unit T4 DNA ligase, 1 mM ATP, 10 mM Tris-Acetate (pH 7.5), 10 mM magnesium acetate and 50 mM potassium acetate]. The ligation mixture was incubated with the restriction fragments at 37°C for 3 hours. The ligase was inactivated at 65 °C for 20 minutes.

Please delete the paragraph beginning on page 27, line 22 and replace with the following:

The ligated DNA target was then amplified by PCR. The PCR mixture contained 12.5 ng ligated DNA, 1 unit AmpliTaq Gold polumerase (Perkins Elmer), 0.272 mM EcoRI selective primer (5'-AAGGGGTTCGGAATTCCC-3'; (SEQ ID NO: 12) CC as the selective bases), 0.272 uM Sau3AI selective primer (5'-TCACTATAGGGCGATCTG-3'; (SEQ ID NO: 13) TG as the selective bases), 200 uM dNTPs, 15 mM Tris-HCl (pH 8,0), 50 mM KCl, 2.5 mM $MgCl_2$ in a final volume of 50 ul. PCR was performed in a Perkin-Elmer 9600 thermocycler using an initial 10 minute denaturation at 95 °C, 35 cycles of a 1 minute denaturation at 94 °C, annealing for 1 minute at 56 °C and extension at 72 for 2 minutes. This is followed by a final 5 minute extension at 72 °C.

Please delete the paragraph beginning on page 30, line 14 and replace with the following:

Adaptor sequences containing PCR primer templates were then ligated to the DNA sequences in a 10 ul ligation mixture: 1ul DNA solution, 4 ul dH2O, 1 ul 10X T4 DNA ligase buffer, 3 ul 10 mM adaptor [5'-d(GATCCGAAGGGGTTCGAATT)-3' (SEQ ID NO: 14) and 5'-d(pGAATTCGAACCCCTTCGGATC-3') (SEQ ID NO: 15) and 1 ul 400 U/ul T4 DNA ligase] and incubated at 16 °C overnight and then inactivated at 65 °C for 15 minutes. (Figure 7, Step 4)

Please delete the paragraph beginning on page 30, line 20 and replace with the following:

The sequences were amplified in a 25 ul reaction containing 0.25 pmol template DNA, 0.125 units AmpliTaq Gold polymerase (Perkin Elmer), 3 uM primer, [5'-d(GATCCGAAGGGGTTCGAATT)-3' (SEQ ID NO: 16)], 200 uM dNTPs, 15 mM tris-HCl (pH 8.0), 50 mM KCl and 1.5 mM $MgCl_2$.

Please delete the paragraph beginning on page 31, line 16 and replace with the following:

The beads were then resuspended in ligation mixture containing T4 ligase in 1 X T4 ligase buffer and 200 fold excess adaptor I sequence [5'-d(ATTAACCCTCACTAAAGCTGGAG)-3' (SEQ ID NO: 17) and 5'-d(pCTCCAGCTTTAGTGAGGGTTAAT)-3' (SEQ ID NO: 18) BpmI recognition sites are highlighted in boldface] at 16 °C overnight. The ligase was then inactivated by incubation at 65 °C for 10 minutes.

Please delete the paragraph beginning on page 31, line 27 and replace with the following:

A second set of adaptor sequences containing PCR template sequences [5'-d(pCTATAGTGAGTCGTATT-3') (SEQ ID NO: 19) and (5'-AATACGACTCACTATAGNN-3') (SEQ ID NO: 20)] and ligase were then added to the supernatant solution and incubated at 16 °C overnight. The ligase was then heat inactivated at 65 °C for 10 minutes.

Please delete the paragraph beginning on page 32, line 3 and replace with the following:

The samples were then amplified with PCR using T3 (5'-ATTAACCCTCACTAAAG-3') (SEQ ID NO: 21) and T7 5'-d(TAATACGACTCACTATAGGG)-3' (SEQ ID NO: 22) sequencing primers (Operon) in a 50 ml reaction containing 10^6 copies of each target DNA, 1 unit AmpliTaq Gold polymerase (Perkin Elmer), 2 uM each primer, 200 uM dNTPs, 15 mM tris-HCl (pH 8.0), 50 mM KCl and 2.5 mM $MgCl_2$.